

10/538704

- 1 -  
JC17 Rec'd PCT/PTO 10 JUN 2005

SEQUENCE LISTING

<110> The Walter and Eliza Hall Institute of Medical Research

<120> A novel phosphoprotein

<130> 2589867/EJH

<150> AU 2002953341

<151> 2002-12-13

<140> Not yet available

<141> 2002-12-12

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 13

<212> PRT

<213> peptide

<400> 1

Glu Ser Ala Val Ala Glu Ser Arg Glu Glu Arg Met Gly  
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<210> 2

<211> 18

<212> PRT

<213> peptide

<400> 2

Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu  
1 5 10 15

Ser Arg

<210> 3

<211> 18

<212> PRT

<213> peptide

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Arg Arg Ala Ala Ser Met Asp Asn Asn Ser Lys Phe Ala Lys Ser Arg  
1 5 10 15

Ser Arg

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<213> phosphoprotein

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gtgggctgga acctgaccta tagcaggct ggggtgtctg tctgggtgca ggctgtggag 180  
atggatcgga cgctgcacaa gatcaagtgc cgatggagt gctgtatgt gccagccgag 240  
acactctacg acgtcctaca cgacatttag taccgcaaga aatgggacag caacgtcatt 300  
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tgtcccaagc ccctgaagaa ccgtgatgtc atcaccctcc gtcctggct cccatggc 420  
gctgattaca tcattatgaa ctactcagtc aaacatccc aataccacc tcggaaagac 480  
ttggtccgag ctgtgtccat ccagacgggc tacctcatcc agagcacagg gccaagagc 540  
tgcgtcatca cctaccctggc ccaggtggac cccaaaggct cttaccctaa gtgggtgg 600  
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aagtaccccg agtggaaaca gaagcacctg cttacttca agccgtggct gcacccggag 720  
cagagcccg tggccgagcct ggcgtgtcg gagctgtcg tgcagcatgc ggactcactg 780  
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<211> 291  
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Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly Pro Arg Pro Val  
1 5 10 15

Leu Gly Arg Glu Ser Val Gln Val Pro Asp Asp Gln Asp Phe Arg Ser  
20 25 30

Phe Arg Ser Glu Cys Glu Ala Glu Val Gly Trp Asn Leu Thr Tyr Ser  
35 40 45

Arg Ala Gly Val Ser Val Trp Val Gln Ala Val Glu Met Asp Arg Thr  
50 55 60

Leu His Lys Ile Lys Cys Arg Met Glu Cys Cys Asp Val Pro Ala Glu  
65 70 75 80

Thr Leu Tyr Asp Val Leu His Asp Ile Glu Tyr Arg Lys Lys Trp Asp  
85 90 95

Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu Thr Val Asn Ala  
100 105 110

Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro Leu Lys Asn Arg  
115 120 125

Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly Ala Asp Tyr Ile  
130 135 140

Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro Pro Arg Lys Asp  
145 150 155 160

Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu Ile Gln Ser Thr  
165 170 175

Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln Val Asp Pro Lys  
180 185 190

Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser Gln Phe Leu Ala  
195 200 205

Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu Lys Tyr Pro Glu  
210 215 220

Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp Leu His Pro Glu  
225 230 235 240

Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu Ser Val Gln His  
245 250 255

Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu Ser Arg  
260 265 270

Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser Asp Asp Asp Thr  
275 280 285

Ser Leu Thr  
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<210> 6  
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<212> PRT  
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<400> 6

Met Ser Thr Arg Ala Lys Lys Leu Arg Arg Ile Trp Arg Ile Leu Glu  
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20 25 30

Gln Glu Gly Gly Val Thr Ser Ala Ala Ala Ser Thr Leu Ser Glu Pro  
35 40 45

Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg Ala Leu Gly Leu  
50 55 60

Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly  
65 70 75 80

Pro Arg Pro Val Leu Gly Arg Glu Ser Val Gln Val Pro Asp Asp Gln  
85 90 95

Asp Phe Arg Ser Phe Arg Ser Glu Cys Glu Ala Glu Val Gly Trp Asn  
100 105 110

Leu Thr Tyr Ser Arg Ala Gly Val Ser Val Trp Val Gln Ala Val Glu  
115 120 125

Met Asp Arg Thr Leu His Lys Ile Lys Cys Arg Met Glu Cys Cys Asp  
130 135 140

Val Pro Ala Glu Thr Leu Tyr Asp Val Leu His Asp Ile Glu Tyr Arg  
145 150 155 160

Lys Lys Trp Asp Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu  
165 170 175

Thr Val Asn Ala Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro  
180 185 190

Leu Lys Asn Arg Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly  
195 200 205

Ala Asp Tyr Ile Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro  
210 215 220

Pro Arg Lys Asp Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu  
225 230 235 240

Ile Gln Ser Thr Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln  
245 250 255

Val Asp Pro Lys Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser  
260 265 270

Gln Phe Leu Ala Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu  
275 280 285

Lys Tyr Pro Glu Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp  
290 295 300

Leu His Pro Glu Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu  
305 310 315 320

Ser Val Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val  
325 330 335

Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser  
340 345 350

Asp Asp Asp Thr Ser Leu Thr  
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<212> PRT  
<213> human

<400> 7

Met Glu Leu Ala Ala Gly Ser Phe Ser Glu Glu Gln Phe Trp Glu Ala  
1 5 10 15

Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu  
20 25 30

Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys  
35 40 45

Thr Gly Leu His Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser  
50 55 60

Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln  
65 70 75 80

Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu  
85 90 95

Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg  
100 105 110

Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg  
115 120 125

Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly  
130 135 140

Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala  
145 150 155 160

Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe  
165 170 175

Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala  
180 185 190

Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln  
195 200 205

Asn Tyr Leu Lys Lys Thr  
210